Biodiversity of Cyanobacteria and associated microbiome in the BCCM/ULC Culture Collection

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Who are we?

BCCM/ULC is a public culture collection focusing on (sub)polar Cyanobacteria from different ecological origins and their diversity. Currently, it harbours 224 cyanobacterial strains, with 140 being of Antarctic origin. Continuous maintenance of living cultures, most of which are also cryopreserved (as back-up), ensure the preservation and the rapid delivery of strains to clients for fundamental and applied research.

The collection is funded by the Belgian Science Policy Office since 2011 and certified by ISO 9001 for the public deposition and distribution of strains. All available strains can be found in the catalogue: http://bccm.belspo.be/catalogues/ulc-catalogue-search.

Biodiversity

16S rRNA and ITS of the strains are gradually sequenced. For now, the 189 BCCM/ULC strains, for which the 16S rRNA sequences are available, correspond to 75 OTUs (sequences with > 99 % 16S rRNA similarity), and thus, represent a quite large diversity (Figure 1). Morphological identification showed that the strains belong to the orders Synechococcales, Oscillatoriales, Pleurocapsales, Chroococcidiopsidales and Nostocales.

Cyanobacterial culture & their associated microbiome(1)

Purifying non-axenic cultures of Cyanobacteria is a difficult task as they have a tightly associated microbiome, for example, attached to their polysaccharidic sheath. This is a constant problem encountered by cyanobacterial culture collections, which contain therefore many non-axenic isolates. Furthermore, it causes contamination of published cyanobacterial genome sequences by bacterial sequences(2). To recover cyanobacterial genomes and to analyze their microbiome, 17 non-axenic cyanobacterial cultures of the BCCM/ULC collection were selected for metagenomics analysis. The developed pipeline allowed the recovery of 12 (sub)polar and three temperate cyanobacterial genomes. Furthermore, 31 non-cyanobacterial bins were recovered, from which 21 were identified as Proteobacteria and five as Bacteroidetes. Interestingly, some bacterial strains were related even though they were collected from distant sampling sites.

Conclusions

The BCCM/ULC public collection serves as a Biological Resource Centre to conserve *ex situ* and to describe the biodiversity of polar Cyanobacteria. Using metagenomics, it was possible to recover 15 cyanobacterial genomes and in each strain, only one cyanobacterial genome was found proving that the cultures in the BCCM\ULC collection were unicyanobacterial.

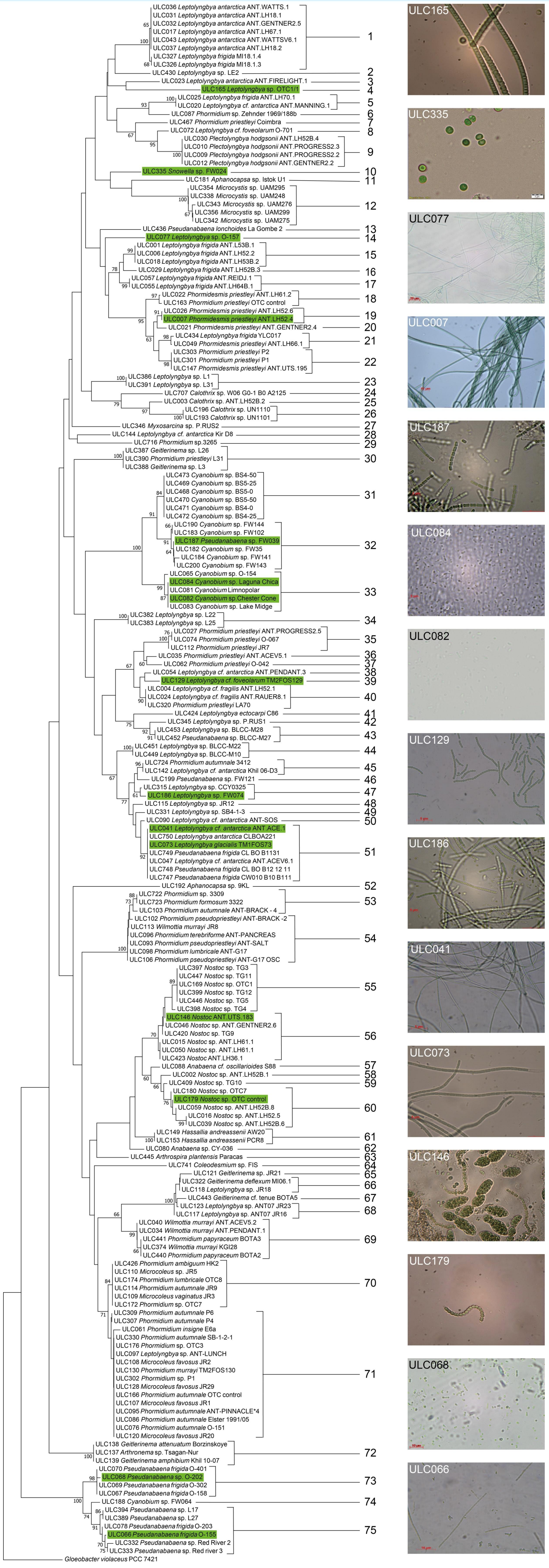

Figure 1. Phylogenetic tree based on 189 16S rRNA sequences of Cyanobacteria of the BCCM/ULC collection with *Gloeobacter violaceus* PCC7421 as outgroup. Isolates, which were used in the metagenomic analysis, are marked in green and are depicted on the pictures. The tree was inferred using MEGA 7 under the NJ algorithm with the Kimura 2 parameter method and gamma distribution.

References: (1) Cornet et al. (2018). Metagenomic assembly of new (sub)polar *Cyanobacteria* and their associated microbiome from non-axenic cultures. Microbial genomics, 4. DOI 10.1099/mgen.0.000212

(2) Cornet et al. (2018). Consensus assessment of the contamination level of publicly available cyanobacterial genomes. PLOS ONE, 13(7): e0200323. DOI 10.1371/journal.pone.0200323

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